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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Jun 04 19:49:29 EDT 2007

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Application No: 10581551

Version No: 1.1

Input Set:**Output Set:****Started:** 2007-06-04 19:49:18.416**Finished:** 2007-06-04 19:49:22.284**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 868 ms**Total Warnings:** 26**Total Errors:** 1**No. of SeqIDs Defined:** 84**Actual SeqID Count:** 84

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 213	Artificial or Unknown found in <213> in SEQ ID (69)
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W 213	Artificial or Unknown found in <213> in SEQ ID (72)
W 213	Artificial or Unknown found in <213> in SEQ ID (73)
W 213	Artificial or Unknown found in <213> in SEQ ID (74)
W 213	Artificial or Unknown found in <213> in SEQ ID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)

Input Set:

Output Set:

Started: 2007-06-04 19:49:18.416
Finished: 2007-06-04 19:49:22.284
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 868 ms
Total Warnings: 26
Total Errors: 1
No. of SeqIDs Defined: 84
Actual SeqID Count: 84

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> MIYAWAKI, ATSUSHI
 KOGURE, TAKAKO
 HAMA, HIROSHI
 KINJO, MASATAKA
 SAITO, KENTA
 KARASAWA, SATOSHI
 ARAKI, TOSHIO

<120> FLUORESCENT PROTEIN

<130> P30056

<140> 10/581,551

<141> 2007-05-25

<150> PCT/JP04/18437

<151> 2004-12-03

<150> JP 2004-018344

<151> 2004-01-27

<150> JP 2003-404472

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<213> Fungia sp.

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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
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35 40 45

aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

tgt tac ggc cac aga cct ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
180 185 190

cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215

<210> 3
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<213> *Fungia* sp.

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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
 145 150 155 160
 Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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 Glu Leu Val Glu Asp Ala Val Ala His Ser
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 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 tgc tac ggc cac aga tgt ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
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145 150 155 160	
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Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met	
165 170 175	
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc	576
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser	
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe						
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp						
145		150		155		160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met						
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser						
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr						
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Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
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Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
				85					90					95		
gag	ttc	gaa	gat	ggt	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
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aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	gtt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
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Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
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tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	gtt	ctg	aag	ggt	gat	gat	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Asp	
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Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Met	
				165					170					175		
aag	act	act	tac	aag	gcg	gca	aaa	aag	att	ctt	aaa	atg	cca	gga	agc	576
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Lys	Ile	Leu	Lys	Met	Pro	Gly	Ser	
			180					185					190			
cat	tac	atc	agc	cat	cgc	ctc	gtc	agg	aaa	acc	gaa	ggc	aac	att	act	624
His	Tyr	Ile	Ser	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr	
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gag	ctg	gta	gaa	gat	gca	gta	gct	cat	tcc	taa						657
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 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
 180 185 190
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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 Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 8

<211> 657

<212> DNA

<213> *Fungia* sp.

<220>

<221> CDS

<222> (1)..(654)

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 20 25 30

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 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

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Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
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 gct tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac	240
Ala Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
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 tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
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 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
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130 135 140	
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
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